

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

SEQUENCE LISTING

<110> Tamatani, Takuya
Tezuka, Katsunari

<120> CELL SURFACE MOLECULE MEDIATING CELL
ADHESION AND SIGNAL TRANSMISSION

<130> 06501-039001

<140> US 09/383,551

<141> 1999-08-26

<150> PCT/JP98/00837

<151> 1998-02-27

<150> JAPAN 09-62290

<151> 1997-02-27

<150> JAPAN 10-62217

<151> 1998-02-26

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 600

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(597)

<400> 1

atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa	48
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys	
1 5 10 15	

gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata	96
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile	
20 25 30	

ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc	144
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val	
35 40 45	

cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat	192
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp	
50 55 60	

ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg	240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu	
65 70 75 80	

aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta 288
 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca 336
 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110
 att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg 384
 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 115 120 125
 cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc 432
 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 130 135 140
 ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt 480
 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
 145 150 155 160
 att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac gac cct 528
 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
 165 170 175
 aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct 576
 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
 180 185 190
 aga ctc aca gat gtg acc cta taa 600
 Arg Leu Thr Asp Val Thr Leu
 195

<210> 2
 <211> 199
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
 1 5 10 15
 Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
 20 25 30
 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
 35 40 45
 Gln Gln Phe Lys Met Gln Leu Lys Gly Gly Gln Ile Leu Cys Asp
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
 65 70 75 80
 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 115 120 125
 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 130 135 140

```

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145                      150                      155                      160
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
                      165                      170                      175
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
                      180                      185                      190
Arg Leu Thr Asp Val Thr Leu
                      195

```

```

<210> 3
<211> 2610
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (26)...(622)

```

```

<400> 3
ggactgttaa ctgtttctgg caaac atg aag tca ggc ctc tgg tat ttc ttt      52
                               Met Lys Ser Gly Leu Trp Tyr Phe Phe
                               1                      5

ctc ttc tgc ttg cgc att aaa gtt tta aca gga gaa atc aat ggt tct      100
Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser
10                      15                      20                      25

gcc aat tat gag atg ttt ata ttt cac aac gga ggt gta caa att tta      148
Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu
                      30                      35                      40

tgc aaa tat cct gac att gtc cag caa,ttt aaa atg cag ttg ctg aaa      196
Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys
                      45                      50                      55

ggg ggg caa ata ctc tgc gat ctc act aag aca aaa gga agt gga aac      244
Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn
                      60                      65                      70

aca gtg tcc att aag agt ctg aaa ttc tgc cat tct cag tta tcc aac      292
Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn
                      75                      80                      85

aac agt gtc tct ttt ttt cta tac aac ttg gac cat tct cat gcc aac      340
Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn
90                      95                      100                      105

tat tac ttc tgc aac cta tca att ttt gat cct cct cct ttt aaa gta      388
Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val
                      110                      115                      120

act ctt aca gga gga tat ttg cat att tat gaa tca caa ctt tgt tgc      436
Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys
                      125                      130                      135

cag ctg aag ttc tgg tta ccc ata gga tgt gca gcc ttt gtt gta gtc      484
Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val

```

140	145	150	
tgc att tgg gga tgc ata ctc att tgg tgg ctc aca aaa aag aag tat			530
Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu Thr Lys Lys Lys Tyr			
155	160	165	
tea tcc agt gtg cac gac cct aac ggt gaa taa atg ttc atg aga gca			580
Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr Met Phe Met Arg Ala			
170	175	180	185
ggg aac aca gcc aaa aaa tct aga ctc aca gat gtg acc cta			620
Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp Val Thr Leu			
190	195		
taatatggaa ctctggcacc caggcatgaa gcacgttggc cagttttcct caacttgaag			682
tgcaagattc tottatttcc gggaccacgg agagtctgac ttaactacat acatctttctg			742
ctgggtgttt gtccaatctg gaagaatgac tgtatcagtc aatggggatt ttaacagact			802
gccttggtac tgccgagtc tctcaaaaaca aacacctctt tgcaaccagc tttggagaaa			862
gcccagctcc tctgtgctca ctgggagtggt aatccctgtc tccacatctg ctccagcaag			922
tgcatcagcc agtaaaaaca acacattttac aagaaaaatg ttttaaaagt gccaggggta			982
ctgaattctg aaagcaaaatg agcagccaaag gaccagctat tctccgcat tcaatctcat			1042
actacctctt ctttctgtag gggtgagaat tctctcttta atcagtcgaag ggagatgctt			1102
caaaagctggr gctattttat ttctgagatg ttgatgtgaa ctgtacatta gtacatactc			1162
agtactctcc ttcaattgct gaaccccaag tgaccatttt accaagactt tagatgcttt			1222
cttgtgcccc caattttctt tttaaaaata cttctacatg actgcttgac agcccaacag			1282
ccactctcaa tagagagcta tgtcttacct tctttcctct gctgctcaat agttttatat			1342
atctatgcat acatatatac acacatatgt atataaaaatt cataatgaat atattttgctt			1402
atattctccc tacaagaata tttttgctcc agaaaagacat gttcttttct caaattcagt			1462
taaaaatgggt tactttgttc aagttagtggt taggaaacat tgccccgaat tgaaaqcaaa			1522
tttawtttat ttacctatct totaccatta totatgtttt catgggtgcta ttaattacaa			1582
gcttagttct tttgttagat catattaaaa ttgcaaaaca aatcatcttt aatggggccag			1642
catctctcat gggtagagca gaatattcat ttgacctgaa agctgcagtt actataggct			1702
gctgtcagac tatacccatg gtgcctctgg gcttgacagg tcaaaaatgg ccccatcagc			1762
ctggagcagc cctccagacc tgggtggaat tccagggttg agagactccc ctgagccaqa			1822
ggccactagg tattcttgct cccagaggct gaagtcaccc tgggaatcac agtggctctac			1882
ctgcattcat aattccagga tctgtgaaga gcacatatgt gtcaggccac aattccctct			1942
tataaaaaacc acacagcctg gaaattggcc ctggcccttc aagatagcct tctttaaat			2002
atgatttggt tagaaaagatt cttaaatatg tggaaatatga ttattcttag ctggaatat			2062
ttctctactt cctgtctgca tgcccaaggc ttctgaagca gccaatgtcg atgcaacaac			2122
atttgtaact ttaggtaaac tgggattatg ttgtagtta acattttgta actgtgtgt			2182
tatactttac aagttagacc cgatatgtca ttatgcatac ttatattatc ttaagcatgt			2242
gtaatgctgg atgtgtacag tacagtacwt aacttgtaat ttgaatctag tatgggtgtc			2302
tgttttcagc tgacttggaac aacctgactg gctttgcaca ggtgttccct gagtgtgtg			2362
caggttttctg tgtgtgggggt ggggtatggg gaggagaacc ttcatgggtg cccacctggc			2422
ctgggtgtcc aagctgtgcc tcgacacatc ctcatcccaa gcatgggaca cctcaagatg			2482
aataataatt cacaaaattt ctgtgaaatc aaatccagtt ttaagaggag ccacttatca			2542
aagagatttt aacagtagta agaaggcaaa gaataaacat ttgatattca gcaactgaaa			2602
aaaaaaaa			2610

<210> 4
 <211> 2072
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (35)...(634)

<400> 4

ctggaggaggga agagtgccagc tcttccctggc agac atg aag ccc tac ttc tgg tgc 55
Met Lys Pro Tyr Phe Ser Cys
1 5

gtc ttc gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctc aat 103
Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn
10 15 20

gac ttg gcc aat cac agg atg ttt tgg ttt cac gat gga ggt gta cag 151
Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln
25 30 35

att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg 199
Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
40 45 50 55

ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc 247
Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser
60 65 70

gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg 295
Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu
75 80 85

tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag 343
Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln
90 95 100

ggc agc tac ttt tta tgc agc ctg tgg att ttc gac cca ccc cct ttt 391
Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe
105 110 115

caa gaa aag aac ctt agt gga gga tat tgg ctt att tat gaa tcc cag 439
Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln
120 125 130 135

ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt 467
Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe
140 145 150

gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa 535
Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys
155 160 165

aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc 583
Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe
170 175 180

atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt atg acc 631
Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Met Thr
185 190 195

tca taatctggaa cacgggaacc catggaggaa ctacactgtc tagttccct 684
Ser
200

```

gaaacttgaa tggagaaaagt cttctatctt cttggaccaca gggcatctga cttgattaac 744
tactgatacc tcttttggk gttttgtttg tctggatcag tgactatcag tcaactcggaa 804
tttcagcaga ctgcccctggg tttgctgagt ctttttaagg caaacccctt cttatagaaq 864
accgggctca tatgtattca acaaacagac ctcaactggga tacaatcccc tctttctgag 924
cctgcttcta gctatgcacc ggccagcaag acaaacatat ctccagcatt tttacaaaaa 984
tggcagggtg tgaatctgta aagtacacag gcagccattg accaccgtct gtccctcgtt 1044
tttcagattc tatttttttc catagagatc agcatttctt ctagaatcag acagtagagg 1104
tagatgcttc acaacagaaq cttctatgtt tctgagatgt tgatgaattc atgctttagt 1164
accaccatgt tctctaacaa cttctatatt ccagctgato actgcttcag ggtttagatg 1224
cctgcttttg ctttcaagtc tccccctaaa gatactccca caggctctact tgggtggcctg 1284
cagccactct gaattaggaaq tttggcttac aatttccccc cttctgctgt caaaaaaaaaa 1344
aattagtaga tatgattttt ccatattttt cctgccaaag taattttttt cagcaaaagac 1404
atctaaattc agttaatatg gtttactgtg ttgatattag tggcagtaaa cattttctcag 1464
aatcaaaaagc aaattaattt tgcgggtggg tttttctacc atttatcttg gtttccatgg 1524
tgctattact cacaagttta gctatttttt tatgcatcat attaaagttg caagcaagca 1584
gagcaaccct cggttaatgg gcaaacattc tcttggggta gaatgaattg tctatttagc 1644
ccgaaaactg cagttttctgt ggggtggctgc cagactacag ccgtgctttg ctctggcttt 1704
gacaggttga aatagycctc atgascstgg aacagwactc cagactgtgc tggagtccca 1764
aagttaggag ggccatggag cctgggacag gctgctgctt tggctcttag gatctaggaa 1824
raattacaga ggggccaaga cagagttccc tccccctaga actgtgcagg ctggaaqtca 1884
ggccctggcac ttttaagatag ctttcttttag aacatgagtt agttggtagt attctgacct 1944
gtaaacagcc tatkgttgct cggagcttga ccattttctt cacttccctg tctgcatgcc 2004
taagacttct agagcagcca acgtatatgc aacattaaag aaaaaaaaaa aaaaaaaaaa 2064
aaaaaaaaa 2072

```

<210> 5
 <211> 603
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)... (600)

```

<400> 5
atg aag cag tac ttc tgc cat gtc ttc gtc ttc tgc ttc cta atc aga 48
Met Lys Pro Tyr Phe Cys His Val Phe Val Phe Cys Phe Leu Ile Arg
1 5 10 15

ctt tta aca gga gaa atc aat ggc tgg gcc gat cat agg atg ttt tca 96
Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
20 25 30

ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc 144
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
35 40 45

cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa 192
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50 55 60

ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca 240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
65 70 75 80

atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta 288

```

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc 336
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
100 105 110

att ttc gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat 384
Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115 120 125

tgg cat att tat gaa tcc cag ctg tgc tgc cag ctg aag ctg tgg cta 432
Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

ccc gta ggg ttg cca gct ttc gtt gtg gta ctg ctt ttt gga tgc ata 480
Pro Val Gly Leu Pro Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac 528
Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag 576
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

tct aga ctt gca ggt gtg acc tca taa 603
Ser Arg Leu Ala Gly Val Thr Ser
195 200

<210> 6
<211> 836
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (35)...(682)

<400> 6
ctggagggga agagtgcagc tgttcctggc agac atg aag ccc tac ttc tgc tgc 55
Met Lys Pro Tyr Phe Ser Cys
1 5

gtc ttt gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctg aat 103
Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn
10 15 20

gac ttg gcc aat cac agg atg ttt tgg ttt cac gat gga ggt gta cag 151
Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln
25 30 35

att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg 199
Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
40 45 50 55

ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc 247
 Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser
 60 65 70

gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg 295
 Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu
 75 80 85

tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag 343
 Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln
 90 95 100

ggc agc tac ttt tta tgc agc ctg tgg att ttc gac cca ccc cct ttt 391
 Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe
 105 110 115

caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag 439
 Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln
 120 125 130 135

cct tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt 467
 Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe
 140 145 150

gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa 535
 Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys
 155 160 165

aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc 583
 Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe
 170 175 180

atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt aca gca 631
 Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Thr Ala
 185 190 195

ccc ctt agg gct ttg ggg aga gga gaa cac tct tca tgt caa gac cgg 679
 Pro Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg
 200 205 210 215

aat taatttggtt atttctatgt taaaagaaaag acattttttt ccttaaagat 732
 Asn

aatttttgta tttttatgtg aaagtctgaa ttttcatttt aactcgactt atatactctg 792
 tggatatatta aaaataatgt ttgtgaaaaa aaaaaaaaaa aaaa 836

<210> 7

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 7

ttgctctgaga tgaagcccta ctctctg

<210> 9
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 9
 accctacggg taacggatcc ttcagctggc aa

32

<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 9
 taactgttcc tggagaacat gaagtcaggc

30

<210> 10
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 10
 atcctatggg taacggatcc ttcagctggc

30

<210> 11
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 11
 cgtgatattg ctgaagagct tggcggccga tgggc

35

<210> 12
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 12
 cattcaagtt tcagggaact agtccatggc ttcc

34

<210> 13
 <211> 200
 <212> FRT
 <213> Rattus norvegicus

<400> 13
 Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys
 1 5 10 15
 Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
 20 25 30
 Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val
 35 40 45
 Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
 65 70 75 80
 Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr
 115 120 125
 Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
 130 135 140
 Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile
 145 150 155 160
 Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp
 165 170 175
 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
 180 185 190
 Ser Arg Leu Ala Gly Met Thr Ser
 195 200

<210> 14
 <211> 200
 <212> PRT
 <213> Mus musculus

<400> 14
 Met Lys Pro Tyr Phe Cys His Val Phe Val Phe Cys Phe Leu Ile Arg
 1 5 10 15
 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
 20 25 30
 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
 35 40 45
 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
 65 70 75 80
 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
 115 120 125
 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
 130 135 140

```

Pro Val Gly Leu Pro Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145          150          155          160
Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
          165          170          175
Pro Asn Ser Glu Tyr Met Phe Met Ala Val Asn Thr Asn Lys Lys
          180          185          190
Ser Arg Leu Ala Gly Val Thr Ser
          195          200

```

<210> 15
 <211> 216
 <212> PRT
 <213> Rattus norvegicus

```

<400> 15
Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys
1          5          10          15
Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
          20          25          30
Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val
          35          40          45
Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp
          50          55          60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
65          70          75          80
Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
          85          90          95
Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser
          100          105          110
Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr
          115          120          125
Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
          130          135          140
Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile
145          150          155          160
Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp
          165          170          175
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
          180          185          190
Ser Arg Leu Ala Gly Thr Ala Pro Leu Arg Ala Leu Gly Arg Gly Glu
          195          200          205
His Ser Ser Cys Gln Asp Arg Asn
          210          215

```

<210> 16
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> (1)...(200)
 <223> Xaa = Any Amino Acid

<400> 16

```

Met Lys Pro Tyr Phe Xaa Xaa Val Phe Val Phe Cys Phe Leu Ile Lys
1      5      10      15
Leu Leu Thr Gly Glu Xaa Asn Xaa Xaa Ala Asn His Arg Met Phe Ser
20      25      30
Phe His Xaa Gly Gly Val Gln Ile Ser Cys Xaa Tyr Pro Glu Thr Val
35      40      45
Gln Gln Leu Lys Met Gln Leu Phe Lys Xaa Arg Glu Val Leu Cys Asp
50      55      60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
65      70      75      80
Met Xaa Cys Xaa Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85      90      95
Xaa Asn Xaa Asp Ser Ser Gln Gly Ser Tyr Xaa Xaa Cys Ser Leu Ser
100     105     110
Ile Phe Asp Pro Pro Pro Phe Gln Glu Xaa Asn Leu Ser Gly Gly Tyr
115     120     125
Leu Xaa Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130     135     140
Pro Val Gly Cys Ala Ala Phe Val Xaa Xaa Leu Leu Phe Gly Cys Ile
145     150     155     160
Xaa Ile Xaa Trp Phe Xaa Lys Lys Lys Tyr Xaa Ser Ser Val His Asp
165     170     175
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180     185     190
Ser Arg Leu Ala Gly Xaa Thr Xaa
195     200

```

<210> 17

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> (1)...(214)

<223> Xaa = Any Amino Acid

<400> 17

```

Met Leu Xaa Leu Xaa Leu Ala Trp Xaa Leu Xaa Leu Phe Xaa Leu Xaa
1      5      10      15
Ile Xaa Val Xaa Xaa Xaa Xaa Ile Xaa Val Xaa Gln Xaa Xaa Xaa Xaa
20      25      30
Xaa Ala Xaa Xaa Asn Gly Xaa Xaa Xaa Xaa Xaa Cys Lys Tyr Xaa Xaa
35      40      45
Pro Xaa Xaa Xaa Xaa Glu Phe Arg Xaa Xaa Leu Leu Lys Gly Xaa Asp
50      55      60
Ser Xaa Val Xaa Xaa Cys Xaa Xaa Xaa Xaa Thr Tyr Xaa Xaa Gly Asn
65      70      75      80
Xaa Val Xaa Xaa Lys Xaa Xaa Xaa Xaa Cys Xaa Gly Xaa Leu Ser Asn
85      90      95
Asn Ser Val Xaa Phe Xaa Leu Gln Asn Leu Xaa Xaa Xaa Xaa Thr Xaa
100     105     110
Xaa Tyr Phe Cys Lys Xaa Glu Xaa Met Tyr Pro Pro Pro Tyr Xaa Xaa
115     120     125
Xaa Xaa Xaa Asn Gly Thr Xaa Ile His Val Xaa Xaa Xaa Xaa Leu Cys

```

```

      130      135      140
Pro Xaa Xaa Xaa Phe Xaa Xaa Trp Xaa Leu Xaa Xaa Val Xaa Xaa Xaa
145      150      155      160
Leu Xaa Xaa Tyr Ser Xaa Leu Xaa Thr Ala Xaa Ile Xaa Xaa Xaa Xaa
      165      170      175
Xaa Lys Lys Arg Ser Xaa Leu Xaa Xaa Gly Xaa Tyr Met Xaa Met Xaa
      180      185      190
Pro Xaa Xaa Pro Xaa Xaa Xaa Xaa Lys Xaa Xaa Gln Pro Tyr Xaa Xaa
      195      200      205
Asp Phe Xaa Xaa Xaa Xaa
      210

```

```

<210> 18
<211> 6
<212> PRT
<213> Homo sapiens

```

```

<400> 18
Met Tyr Pro Pro Pro Tyr
  1             5

```

```

<210> 19
<211> 4
<212> PRT
<213> Homo sapiens

```

```

<400> 19
Tyr Met Asn Met
  1

```

```

<210> 20
<211> 4
<212> PRT
<213> Homo sapiens

```

```

<400> 20
Tyr Val Lys Met
  1

```

```

<210> 21
<211> 6
<212> PRT
<213> Homo sapiens

```

```

<400> 21
Phe Asp Pro Pro Pro Phe
  1             5

```

```

<210> 22
<211> 4
<212> PRT
<213> Homo sapiens

```

```

<400> 22
Tyr Met Phe Met
  1

```

<210> 23
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> (1)...(216)
 <223> Xaa = Any Amino Acid

<400> 23
 Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys
 1 5 10 15
 Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
 20 25 30
 Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val
 35 40 45
 Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
 65 70 75 80
 Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr
 115 120 125
 Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
 130 135 140
 Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile
 145 150 155 160
 Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp
 165 170 175
 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
 180 185 190
 Ser Arg Leu Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 210 215

<210> 24
 <211> 16
 <212> PRT
 <213> Rattus norvegicus

<400> 24
 Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg Asn
 1 5 10 15

<210> 25
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 25

```

Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1      5      10
Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35      40      45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Gln
50      55      60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65      70      75
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85      90      95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100      105      110
Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser
115      120      125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130      135      140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145      150      155      160
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
165      170      175
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
180      185      190
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
195      200      205
Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
210      215      220

```

<210> 26

<211> 223

<212> PRT

<213> Homo sapiens

<400> 26

```

Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1      5      10
Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20      25      30
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35      40      45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50      55      60
Lys Ala Tyr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65      70      75      80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr
85      90      95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100      105      110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115      120      125
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
130      135      140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145      150      155      160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165      170      175

```


Tyr	Ser	Phe	Leu	Leu	Thr	Ala	Val	Ser	Leu	Ser	Lys	Met	Leu	Lys	Lys
			180					185					190		
Arg	Ser	Pro	Leu	Thr	Thr	Gly	Val	Tyr	Val	Lys	Met	Pro	Pro	Thr	Glu
		195					200					205			
Pro	Glu	Cys	Glu	Lys	Gln	Phe	Gln	Pro	Tyr	Phe	Ile	Pro	Ile	Asn	
	210					215					220				